

CLAIMS

1. A method for assessing a cancerous state of a mammal-derived specimen, which comprises:

(1) a first step of measuring a methylation frequency of Fibrillin2 gene contained in a mammal-derived specimen or an index value having the correlation therewith, and

(2) a second step of determining a cancerous state of the specimen based on a difference obtained by comparing the measured methylation frequency or the index value having the correlation therewith, with a control.

2. The assessing method according to claim 1, wherein the mammal-derived specimen is cells.

3. The assessing method according to claim 1, wherein the mammal-derived specimen is a tissue.

4. A method for assessing a cancerous state of a mammal-derived specimen, which comprises:

(1) a first step of measuring a methylation frequency of Fibrillin2 gene contained in the mammal-derived specimen, and

(2) a second step of determining a cancerous state of the specimen based on a difference obtained by comparing the measured methylation frequency with a control.

5. The assessing method according to claim 1, wherein the mammal-derived specimen is cells, and the cancerous state of the specimen is a malignancy of mammal-derived cells.

5 6. The assessing method according to claim 4, wherein the mammal-derived specimen is cells, and the cancerous state of the specimen is a malignancy of a mammal-derived cell.

10 7. The assessing method according to claim 1, wherein the mammal-derived specimen is a tissue, and the cancerous state of the specimen is an amount of cancer cells existing in a mammal-derived tissue.

15 8. The assessing method according to claim 4, wherein the mammal-derived specimen is a tissue, and the cancerous state of the specimen is an amount of cancer cells existing in a mammal-derived tissue.

20 9. The assessing method according to claim 8, wherein the tissue is a pancreatic tissue, and the cancer is pancreatic cancer.

25 10. The assessing method according to claim 1 or 4, wherein the methylation frequency of a gene is a methylation frequency of cytosine in one or more nucleotide sequence(s) represented

by 5'-CG-3' present in a nucleotide sequence of a promoter region,
an untranslated region or a translated region of the gene.

11. The assessing method according to claim 12, wherein
5 the tissue is a pancreatic tissue, and the cancer is pancreatic
cancer.

12. The assessing method according to claim 1 or 4, wherein
the methylation frequency of a gene is a methylation frequency
10 of cytosine in one or more nucleotide sequence(s) represented
by 5'-CG-3' present in a nucleotide sequence of a promoter region
in the gene.

13. The assessing method according to claim 1 or 4, wherein
15 the methylation frequency of a gene is a methylation frequency
of cytosine in one or more nucleotide sequence(s) represented
by 5'-CG-3' present in a nucleotide sequence of an untranslated
region or a translated region of the gene.

20 14. The assessing method according to claim 1, wherein
the methylation frequency of a gene is a methylation frequency
of cytosine in one or more nucleotide sequence(s) represented
by 5'-CG-3' present in the nucleotide sequence represented by
SEQ ID No: 1.

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15. The assessing method according to claim 16, wherein the tissue is a pancreatic tissue, and the cancer is pancreatic cancer.

5 16. A method for assessing a cancerous state of a mammal derived specimen, which comprises:

 (1) a first step of measuring an index value having the correlation with a methylation frequency of Fibrillin2 gene contained in the mammal-derived specimen, and

10 (2) a second step of determining a cancerous state of the specimen based on a difference obtained by comparing the index value having the correlation with the measured methylation frequency with a control.

15 17. The assessing method according to claim 16, wherein the index value having the correlation with a methylation frequency of Fibrillin2 gene is an amount of an expression product of the Fibrillin2 gene.

20 18. The assessing method according to claim 17, wherein the amount of an expression product of Fibrillin2 gene is an amount of a transcription product of the gene.

 19. The assessing method according to claim 17, wherein
25 the amount of an expression product of Fibrillin2 gene is an

amount of a translation product of the gene.

20. A method for searching a substance having the ability of promoting the expression of Fibrillin2 gene, which comprises:

5 (1) a first step of bringing a test substance into contact with a cancer cell,

(2) a second step of measuring an amount of an expression product of Fibrillin2 gene contained in the cancer cell after the first step (1), and

10 (3) a third step of determining the ability of the test substance to promote the expression of Fibrillin2 gene possessed by, based on a difference obtained by comparing the measured amount of an expression product with a control.

15 21. The searching method according to claim 20, wherein the cancer cell is pancreatic cancer cell.

22. An anti-cancer agent, which comprises a substance having the ability found by the searching method of claim 20 as an active ingredient, wherein the active ingredient is formulated into a pharmaceutically acceptable carrier.

23. an anti-cancer agent, which comprises a nucleic acid comprising a nucleotide sequence encoding an amino acid sequence of Fibrillin2 as an active ingredient, wherein the active

ingredient is formulated into a pharmaceutically acceptable carrier.

24. Use of methylated Fibrillin2 gene as a cancer marker.

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25. The use according to claim 24, wherein the cancer marker is a pancreatic cancer marker.

26. A method for inhibiting canceration, which comprises
10 a step of administering a substance which reduces a methylation frequency of Fibrillin2 gene, to cells in a body of a mammal which can be diagnosed as a cancer.

27. The canceration inhibiting method according to claim
15 26, wherein the cancer is pancreatic cancer.